

Archived Editions (COVID-19 Genomics and Precision Public Health Weekly Update)

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COVID-19 Genomics and Precision Public Health Weekly Update Content

- Pathogen and Human Genomics Studies
- Non-Genomics Precision Health Studies
- News, Reviews and Commentaries

Pathogen and Human Genomics Studies

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- Epidemiology and genetic diversity of SARS-CoV-2 lineages circulating in Africa
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We show that after almost one year of the COVID-19 pandemic, only 143 out of the 782 Pango lineages found worldwide circulated in Africa, with five different lineages dominating in distinct periods of the pandemic. Analysis of the number of reported deaths in Africa also revealed large heterogeneity across the continent. Phylogenetic analysis revealed that African viruses cluster closely with those from all continents but more notably with viruses from Europe. However, the extent of viral diversity observed among African genomes is closest to that of the Oceania outbreak, most likely due to genomic under-surveillance in Africa.

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- SARS-CoV-2 B.1.1.7 and B.1.351 spike variants bind human ACE2 with increased affinity. ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1233](#))
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- Identification and trajectory of growth of concerning SARS-CoV-2 variants in Houston, Texas, January through April 2021 based on 11,568 genome sequences ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1238](#))
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- COVID-19 in Amazonas, Brazil, was driven by the persistence of endemic lineages and P.1 emergence ([/PHGKB/phgHome.action?action=forward&dbsource=covUpdate&id=1248](#))
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